I. AMENDMENTS

Amendments to the Specification:

Please replace the paragraph beginning on page 8, line 8 and ending on page 8, line 12 with the following paragraph:

Suitable 5'-UTR sequences for use with the present invention were selected using theoretical sequence analyses and/or experimental methods employing tools such as those available via the Institute of Cytology and Genetics, The Siberian Branch of the Russian Academy of Science (wwwmgsdotbionetdotnscdotru/mgs/programs/leadermrna/ma_mrna_edothtml).

Please replace the paragraph beginning on page 25, line 19 and ending on page 26, line 12 with the following paragraph:

Construction of a modified 5'UTR EPO plasmid (pSC2-2) – To improve the translation efficiency of the recombinant EPO a modified 5' UTR was designed using the translation efficiency algorithm predicting high/low mRNA expression of a mammalian gene (AV. Kochetov, Institute of Cytology and Genetics SD RAS, Russia) available through wwwmgsdotbionetdotnscdotru/mgs/programs/leadermrna/ma_mrna_edothtml. The selected sequence was introduced into the Syn5 primer (Table 1, hereinbelow) which together with the LPG2 primer which corresponds to nucleotides 1416-1440 at the 3' end used to amplify the new 5'-UTR region. In order to increase the translation efficiency the GC content was reduced by introducing via the Syn5 primer a guanine to adenine (G→A) substitution at the third position of the guanine-guanine-guanine triplet encoding glycine at position 2 of SEQ ID NO:10 (see underlined A in SEQ ID NO:3, Table 1, hereinbelow). PCR was performed using pSIC2 plasmid as template DNA and the resultant PCR product was blunt ended using T4 DNA polymerase and was digested with *XbaI*. In parallel, the pSIC2 plasmid DNA was digested with *EcoRI*, blunt ended and digested with *XbaI*. The two DNA fragments were ligated and the resultant plasmid was designated as pSC2-2. Further sequence analysis of the pSC2-2 plasmid revealed the following 5'-UTR sequence: TTTTCTTTTGTTTTGTTTCCACC (SEQ ID NO:6) which is 15-nucleotides shorter at the 5' end than the 5'-UTR sequence introduced in the Syn5 primer: AATTCTTTTGTTTTGTTTTCTTTTGTTTTGTTTCCACC which is set forth by SEQ ID NO:7. The 15-nucleotides deletion was generated by either residual double strand exonucleolytic activity of the T4 DNA polymerase or by a recombination event occurred in the *E. Coli* host cell due to the presence of a highly repetitive sequence. Since the shorter sequence was still scored as having a high translation potential using the translation predicting algorithm is was selected for further use.